

Gencore version 4.5
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OM nucleic - nucleic search, using sw modal

Run on: October 21, 2001, 10:54:58 ; Search time 7124.02 Seconds
 (without alignments)
 11995 940 Million cell updates/sec

Title: US-09-515-806-1

Perfect score: 5525

Sequence: 1 tcgccccac9cgccacc.....aatgcttccatataccctgca 5525

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*

1: gb_ba1:*

2: gb_ba2:*

3: gb_ba3:*

4: gb_in1:*

5: gb_in2:*

6: gb_in3:*

7: gb_on:*

8: gb_ov:*

9: gb_pt1:*

10: gb_pt2:*

11: gb_ph:*

12: gb_p11:*

13: gb_p12:*

14: gb_p13:*

15: gb_p14:*

16: em_ba1:*

17: em_ba2:*

18: em_fun:*

19: em_htgo_hum:*

20: em_htgo_inv:*

21: em_htgo_rid:*

22: em_htg_num1:*

23: em_htg_num2:*

24: em_htg_num3:*

25: em_htg_num4:*

26: em_htg_num5:*

27: em_htg_num6:*

28: em_htg_num7:*

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45: em_pat:*

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84: gb_htg25:*

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86: gb_pr2:*

87: gb_prl:*

88: gb_pr4:*

89: gb_pr5:*

90: gb_pr6:*

91: gb_pr7:*

92: gb_pr8:*

93: gb_pr9:*

94: gb_rol:*

95: gb_rol2:*

96: gb_inv1:*

97: gb_prl0:*

98: em_ba3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1		5156.4	93.3	5163	9	AX056426 Sequence AB037759 Homo sapi AJ243533 Mus muscu AF193343 Mus muscu AF193344 Mus muscu AF193342 Mus muscu AL157497 Homo sapi AK027011 Homo sapi
2		4929.8	89.2	4904	85	
3		3909.8	70.8	5212	94	
4		3896.4	70.5	5230	94	
5		3698.8	66.9	5322	94	
6		3418.4	61.9	5111	94	
7		3332	60.3	3351	93	
8		2949.6	53.4	2986	89	

8

9	2160.4	39.1	2162	93	HSAA43428	Homo sapi
10	1687.6	30.5	1917	93	HSM002022	Ali137676 Homo sapi
11	1081.4	19.6	1138	93	HSM002391	Ali137527 Homo sapi
12	568.8	10.3	157900	66	AC021755	AC021155 Homo sapi
13	568.8	10.3	173364	69	AC025168	AC025168 Homo sapi
14	542.8	9.8	164297	62	AC021238	AC021238 Homo sapi
15	476.2	8.6	61029	78	AC020997	AC020997 Homo sapi
16	406.8	7.4	76861	77	AC087124	AC087124 Mus muscu
17	406.8	7.4	93841	77	AC087124	AC087124 Mus muscu
18	406.8	7.4	13417	77	AC087119	AC087119 Mus muscu
19	242.8	4.4	5721	6	DMU8223	U80223 Drosophila
20	242.8	4.4	5749	5	AF056302	AF056302 Drosophila
21	204.8	3.7	231952	73	AC08641	AC08641 Homo sapi
22	204.4	3.6	38206	87	AC011554	AC011554 Homo sapi
23	201.6	3.6	125290	85	AC05048	AC05048 Homo sapi
24	200.4	3.6	76861	77	AC087122	AC087122 Mus muscu
25	200.4	3.6	128589	77	AC087122	AC087122 Mus muscu
26	200.2	3.6	191352	66	AC020631	AC020631 Homo sapi
27	199.8	3.6	175278	73	AC080932	AC080932 Homo sapi
28	199.8	3.6	181668	64	AC016691	AC016691 Homo sapi
29	198.6	3.6	216497	93	HSDD37C1_0	AL045569 Human DNA
30	197.2	3.6	131692	76	AC07927	AC07927 Homo sapi
31	197.2	3.6	208694	73	AC068037	AC068037 Homo sapi
32	196.2	3.6	188332	69	AC025521	AC025521 Homo sapi
33	196.2	3.6	190239	61	AC009522	AC009522 Homo sapi
34	195.4	3.5	111071	79	AC024591	AC024591 Homo sapi
35	195.4	3.5	145161	79	AL354874	AL354874 Homo sapi
36	195.4	3.5	156703	62	AC011951	AC011951 Homo sapi
37	195.4	3.5	211844	72	AC048370	AC048370 Homo sapi
38	195.2	3.5	42071	85	AC000087	AC000087 Homo sapi
39	195.2	3.5	209039	62	AC011367	AC011367 Homo sapi
40	195	3.5	9701	85	AB01733353	AB01733353 Homo sapi
41	195	3.5	105485	97	HUAC002301	HUAC002301 Homo sapi
42	195	3.5	163847	61	AC009133	AC009133 Homo sapi
43	195	3.5	174582	97	HUAC03010	HUAC03010 Homo sapi
44	195	3.5	182123	60	AC002399	AC002399 Homo sapi
45	194.4	3.5	187711	75	AC073996	AC073996 Homo sapi

ALIGNMENTS

Kazusa DNA Research Institute, Laboratory of DNA Technology,
 4-3 Yana, Kisarazu, Chiba 292-0812, Japan
 (http://odnainfo.kazusa.or.jp, URL: http://www.kazusa.or.jp/huge/),
 +81-438-51-3913, Fax:+81-438-52-3914
 Location/Qualifiers
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 /db_xref="taxon: 9606"
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 IVSVALPEKLASLQKQFLLQVPLVQVQHNGIKAQDQHETLQKQFLLKDDAARGPA
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BASE COUNT ORIGIN	1449	a	1130	c	1198	g	1217	t
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Matches 4931; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

62 TCCAGCATGAGATTCAAGAGAGAAAGAGATAAAAGAAGAGAAAAGGAAAGAAA 121

706 aggaccaggacacagaacaaacggctccattctacatggaggctctctgtactttgtag 765

182 AGGACCCAGGAGGACACAGAACGGCTGCCATTCTACATGGGGCTCTCTGACTTTGTAG 241

242 GAAATGGTAAACATCGGGCAAACTCCCTCAGGAAGGCTCTAGGGAGAACCTCAGTATTCTG 301

Qy	777	catcgccaaactcctcagaaggctctaggcagagaacgtcagtttctgtatgttaatgt	836
Db	807	GCCCGACATACTCTCAGGAAGCTCAGGCCAGAACCTCAGTATTCAGTGTAGTGGT	866
Qy	837	gaaggattctctggcttctgtaaaatttgttatttgttatttgttatttgttatttgttattgt	896
Db	867	GAACCTCTCTGGTCAGCTGGCCATCCCTCCATTCCTGTGGTACGCCCTATAGCTC	926
Qy	897	atggcacaaggaaatgttattggcgtatgtgaacaacttggaaataattgtctacaat	956
Db	927	ATGGCACAAGGGAGATGTTGCAUTGANTGAGCCTGGAAANGTGTATTCATAAT	986
Qy	957	qcttggaaaacgcactgtggctttgtttgtttatgtatgtggctcttcoagtgcag	1016
Db	987	GCTTGAAAAGCCACGGCAGCTTGTCTCATGAGTCATGGTGCCTTCAGTGGCGAG	1046
Qy	1017	aaaaaatggctttaccatccatggaaattgttataatggcaaaagg	1076
Db	1047	-- -AGATGGCCCTTGCCCTTACAGTCAGAGAAAAGTGCAGAAAGGG	1103
Qy	1077	catttcaaggaaacaaacgaaatgttcaactcaacttggaaaattgtggccatccaaatgt	1136
Db	1104	CAGATTCAGAGCAGAACAGATTCAGTCCTCTGAACTTGACACTGACCTCCATATC	1163
Qy	1137	gtacccttacccatgtcaatgtatctcaaaaggcaacgcactcoatctgtggacat	1196
Db	1164	GTCCTACTTGGCATGACTTCAGTCAGAGGGAGGACTCCATTGTATGACATCTG	1223
Qy	1197	gtggggcacattttgtggatgtggatgtggatgtggatgtggatgtggatgtggat	1256
Db	1224	GCAGGCACTTCAGGGCATCTCTGGCTACACACCTGAGCCACGGCCCACTGCC	1283
Qy	1257	gtgtctcgttccaggatcacatgttcgttccaggatgttcgttccaggatgttcgt	1316
Db	1284	GCCACCAAGCTGGCCAAATACARAGCCAGGCTGAAAGGCTGAACTTACAGC	1343
Qy	1317	aatttgttgtcataaaggctctgttgtcatatgttttgttgttgttgttgttgttgt	1376
Db	1344	AACCTGGTGTGCAAAAGTCATGTCAGCAGTCAGTCAGTCAGTCAGTCAG	1403
Qy	1377	gtcaaggatcacggactataggatccatgtttttatgttgttgttgttgttgttgt	1436
Db	1404	GTCAGATAACAGACTACAGCACTCTTAAGGCTGCTGAACTGAGGATGTAA	1463
Qy	1437	tttggcaaaacccatgttgtttttatgttgttgttgttgttgttgttgttgttgt	1496
Db	1464	TTTCAGCAAGCTGCTGTTAGTACAGTCACTGCTGCTGCTGCTGCTGCTG	1523
Qy	1497	ggatgttgttgttgttgttgttgttgttgttgttgttgttgttgttgttgttgttgttgt	1556
Db	1524	GGGATGTGTGGCCCTGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGG	1583
Qy	1557	gatgtccatgttgttgttgttgttgttgttgttgttgttgttgttgttgttgttgttgt	1616
Db	1584	GAGTACCTGGT	1703
Qy	1617	tgttgtgttgttgttgttgttgttgttgttgttgttgttgttgttgttgttgttgttgt	1676
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Qy	1737	gatttgttgttgttgttgttgttgttgttgttgttgttgttgttgttgttgttgttgt	1796
Db	1764	GACTACATGAGCCATCCAGAAACAGCTCCAGAACGGCTCCACAGCTGCTG	1823
Qy	1797	acacgacacacgtttcccgactactcatgttgttgttgttgttgttgttgttgtaa	1856
Db	1824	ACAGAAACAGTCCTGGFACTTCATTCAGTGTGAAACTAACCTCTAGGAAA	1883

erman Genome Project.
his clone (DKFZp34H149) is available at the RZPD in Berlin.
Please contact the RZPD, Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY. Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at <http://www.molbioc.biocenter.uni-bamberg.de/clone/>

FEATURES	source	Query Match	Score	DB	Length	Location/Qualifiers
1. 1917		Qy 4151	agctctggggccaggttccactgcattgggttcacgcatagtctatggacaatataatctgc	4210		
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DH10B; sites NotI + Sali"		Qy 4271	tgttgccatggatgtctatgtccaggggccatcaacccatggaaactctgcacgagg	4330		
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polyA_signal		Qy 4391	cagacatcatggaaaatccacctatgtggccctgttccggataaagaaaggatctgt	4450		
POLY_A SITE	1907	Db 961	CAGACATCATGAAATCCATAGTGGCCCTTGTCTCGATAAGAAGGACATGCA-	1019		
BASE COUNT	612 a	Qy 4451	ggtaatgttttgcggatggatggatggcggatggatggatggatggatggatgt	4510		
ORIGIN	376 c	Db 1020	-----	-----	1019	
Best Local Similarity	91.18;	Qy 4511	ggaccatgtactgcaggaaactgtggatggatggatggatggatggatggatgt	4570		
Matches 1903; Conservate	0;	Db 1020	-----	-----	-----	
Pred. No. 0;	Mismatches	Qy 4571	ttccgatataatctgcagtgcacaaatctgtggaaatgggttcataatgccttcagg	4630		
4;	Indels	Db 1028	TTCCGATAATCTTGCACTGCAGTGCAGTCAGTCTCAGGTTCTGTT	1087		
5;	Gaps	Qy 4631	tggaaatccatggagccaaatgggttcocattgtggatgttgcgtccggagaatgtc	4690		
		Db 1088	TGAAATCCTATGGACACAGTGGTTCCATGTGACTGTGTAGGCCAGAAAGTGT	1147		
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		Qy 4751	caacttacatggaaaatggatgtggatgtggatgtggatgtggatgtggatgt	4810		
		Db 1179	-----	-----	-----	
		Qy 4811	aatattacacgttttatcatggatgtggatgtggatgtggatgtggatgtggat	4870		
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		Qy 4871	gaagcagactgtgttgcacgcataatggatgtgtgtgtgtgtgtgtgtgtgt	4930		
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		Qy 4931	ttataacatggaaaatggatgtggatgtggatgtggatgtggatgtggatgtggat	4990		
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		Qy 4991	ctactacagaaatctttaaacccatggaaaactgtgtgtgtgtgtgtgtgtgtgt	5050		
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		Qy 5051	aggcttactgtggaaataatggatgtggatgtggatgtggatgtggatgtggat	5110		
		Db 1439	AGGCTTATACGGATAATGGTGTGTTGACATCCTCATATAATTAAATTAAATT	1498		
		Qy 5111	gaagggtctgggtgcgtggatgtggatgtggatgtggatgtggatgtggatgtggat	5170		
		Db 1499	GAAGGGCTGGGSCAGTGGCTCACCTTAACTCCACACTTGGAGGCCAGGGAG	1558		
		Qy 5171	gaagactgtgttgcacccaggatgtggatgtggatgtggatgtggatgtggatgtggat	5230		
		Db 1559	GAAGACTGTGTTGAAACAGAGCTGCTGAGCTGAGCTGAGCTGAGCTGAG	1618		
		Qy 5231	CTataaaaactaa	-----	-----	

FEATURES	source	BASE COUNT	ORIGIN	Query Match	Score	Length	Best Local	Similarity	Length	Matches	Conservative	0;	Mismatches	2;	Indels
*		76768	76867:	76867: gap of unknown length											
*		76868	79623:	79623: contig of 2756 bp in length											
*		79624	79723:	79723: gap of unknown length											
*		79724	90362:	90362: contig of 10639 bp in length											
*		90363	90462:	90462: gap of unknown length											
*		90463	93120:	93120: contig of 2558 bp in length											
*		93021	93120:	93120: gap of unknown length											
*		93121	157900:	157900: contig of 64780 bp in length.											
			Location/Qualifiers												
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			/chromosome="15"												
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			/clone="RP1-521C20"												
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			/note="This clone overlaps RP1-43D14 and RP1-43D15."												
		43137	a	35607	c	36148	g	42500	t	508	others				

Quality coverage: 10.2x in Q20 bases; sum-of-contigs

Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than an error in 10,000 bp.

Base-quality values are not generally visible from the Genbank flat file format but are available as part of this entry's ASN.1 file.

NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1	67961	contig of 67961 bp in length
1	67962	gap of unknown length
1	68062	contig of 8706 bp in length

Quality coverage: 10.2x in Q20 bases; sum-of-contigs
Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality 20. Quality levels above 40 are expected to have less than error in 10,000 bp. Sequence-by-base quality values are not generally visible from the Genbank flat file format but are available as part of this entry's ASN.1 file.

NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have

RESUME
AC025168/C
LOCUS
DEFINITION Homo sapiens chromosome 15 clone RP11-43D14 map 15q14, ***
SEQUENCING IN PROGRESS ***, 1 ordered pieces.
ACCESSION AC025168
VERSION AC025168.6
GT:1362123

KEYWORDS	HTG; HTGS_PHASE2; HTGS_FULLTOP.
SOURCE	human.
ORGANISM	<i>Homo sapiens</i>
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S., Burke, J., Dors, M., Fleetwood, P., Kaur, A., Madan, A., Nesbitt, R., Pate, D. and Hood, L.
TITLE	Sequencing of human chromosome 15 D15S146-D15S117 region unpublished
JOURNAL	2 (bases 1 to 173364)
REFERENCE	Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S., Dors, M., Dickhoff, R., Fleetwood, P., Harrison, G., James, R., Kaur, A., Madan, A., Owen, M. P., Ratcliffe, A., Shaffer, T., and Hood, L.
JOURNAL	Submitted (07-MAR-2000) Multimegabase Sequencing Center, University of Washington, PO Box 357730, Seattle, WA 98195, USA
COMMENT	On Apr 13, 2001 this sequence version replaced gi:10305066.
-----	Genome Center
Center	Multimegabase Sequencing Center
Center code	UWMS
Web site	http://chroma.mbt.washington.edu/msg9_www
Contact	lerowen@systemsbiology.org
-----	Summary Statistics
Sequencing vector	pUC18; L08752
Chemistry	Dye-terminator
Chemistry	Big Dye; 90% of reads
Chemistry	Dye-primer
Assembly program	Phrap; version 0.990399
Insert size	172000; agarose-fp
Quality coverage	12.6x in Q20 bases; sum-of-contigs
-----	Sequence Quality Assessment:
	This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
	All manually edited bases have been reduced to quality zero.
	Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
	Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
-----	* NOTE: This is a 'working draft' sequence. It currently consists of 1 contig. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
	* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
	* the accession number will be preserved. Homo sapiens, clone RP11-173364; contig of 173364 bp in length.
FEATURES	Location/Qualifiers
source	1. 173364: contig of 173364 bp in length.
ORIGIN	1. 173364: contig of 173364 bp in length.
BASE COUNT	51234 a 35556 c 35550 g 51004 t
ORIGIN	Query Match 10.3%; Score 568.8; DB 69; Length 173364;
Best Local Similarity 99.7%; Pred. No. 1.8e-10.3;	0; Mismatches 0; Indels 0; Gaps 0;
Matches 570; Conservative	0;
Qy 4953 aagggtgtgtgtatttttcttacatgtactactatcagaatccatttttaa 5012	
Db 5279 AGGGTGTGTGTCTTACATTCGTACTAGATGACTACTAGAATCTTATTATAA 5220	

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 Project Information
 Center project name: L3086
 Center clone name: 10_K15

----- Summary Statistics
 Sequencing vector: M13; M7815; 98% of reads
 Consensus quality: 142640 bases at least Q40
 Consensus quality: 152432 bases at least Q30
 Consensus quality: 157096 bases at least Q20
 Insert size: 153000; agarose-fp
 Insert size: 160597; sum-of-concings
 Quality coverage: 3.4 in Q20 bases; agarose-fp

NOTE: This is a 'working draft' sequence. It currently
 * consists of 34 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

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 * 1165 2366: contig of 1202 bp in length
 * 2367 2466: gap of 10 bp
 * 2467 3540: contig of 1074 bp in length
 * 3541 3640: gap of 10 bp
 * 3641 4861: contig of 1221 bp in length
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 * 4962 5968: contig of 1007 bp in length
 * 5969 6068: gap of 100 bp
 * 6069 7242: contig of 1174 bp in length
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 * 7343 8453: contig of 1111 bp in length
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 * 8554 9820: contig of 1267 bp in length
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 * 20813 20912: gap of 100 bp
 * 20913 24906: contig of 3944 bp in length
 * 24907 25006: gap of 100 bp
 * 25007 28926: contig of 3990 bp in length
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 * 29027 34159: contig of 5133 bp in length
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 * 104194 112355: contig of 8202 bp in length
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 * 123345 135427: contig of 12083 bp in length
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VERSION AC090997.1 GI:113431057
 SOURCE HTG; HTGS_PHASE0.
 ORGANISM Homo sapiens
 JOURNAL
 REFERENCE AUTHORS Birren, B., Linton, L., Nusbaum, C., and Lander, E.
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; HOMO.
 1 (bases 1 to 61029)
 Birren, B., Linton, L., Nusbaum, C., and Lander, E.
 Homo sapiens chromosome 15, clone RP11-521C20
 Unpublished
 2 (bases 1 to 61029)
 Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S.,
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 Retta, R., Rieback, M., Riley, R., Ruse, C., Rogoz, P., Roman, J.,
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 Theodore, J., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
 Viei, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
 Zainoun, J., Zembik, L., Zimmer, A., and Zody, M.
 Direct Submission (22-MAR-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIIR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L13141
 Center clone name: 521_C_20

 * NOTE: This record contains 92 individual
 * sequencing reads that have not been assembled into
 * contigs. Runs of N are used to separate the reads
 * and the order in which they appear is completely
 * arbitrary. Low-pass sequence sampling is useful for
 * identifying clones that may be gene-rich and allows
 * overlap relationships among clones to be deduced.
 * However, it should not be assumed that this clone
 * will be sequenced to completion. In the event that
 * the record is updated, the accession number will
 * be preserved.
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 * 671 1297; contig of 627 bp in length
 * 1298 1397; gap of 100 bp
 * 1398 2087; contig of 690 bp in length
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 * 2188 2956; contig of 769 bp in length
 * 2957 3056; gap of 100 bp
 * 3057 3690; contig of 634 bp in length
 * 3691 3790; gap of 100 bp
 * 3791 4405; contig of 615 bp in length
 * 4406 4505; gap of 100 bp
 * 4506 5161; contig of 656 bp in length
 * 5162 5261; gap of 100 bp
 * 5262 5867; contig of 606 bp in length
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* * 58868 5967: gap of 100 bp
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* * 1967188 197595: contig of 778 bp in length
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* * 2023195 203195: gap of 100 bp
* * 2031196 203995: contig of 782 bp in length
* * 2039197 204795: gap of 100 bp
* * 2047198 205595: contig of 783 bp in length
* * 2055199 206395: gap of 100 bp
* * 20631200 207195: contig of 784 bp in length
* * 20711201 207995: gap of 100 bp
* * 20791202 208795: contig of 785 bp in length
* * 20871203 209595: gap of 100 bp
* * 20951204 210395: contig of 786 bp in length
* * 21031205 211195: gap of 100 bp
* * 21111206 211995: contig of 787 bp in length
* * 21191207 212795: gap of 100 bp
* * 21271208 213595: contig of 788 bp in length
* * 21351209 214395: gap of 100 bp
* * 21431210 215195: contig of 789 bp in length
* * 21511211 215995: gap of 100 bp
* * 21591212 216795: contig of 790 bp in length
* * 21671213 217595: gap of 100 bp
* * 21751214 218395: contig of 791 bp in length
* * 21831215 219195: gap of 100 bp
* * 21911216 219995: contig of 792 bp in length
* * 21991217 220795: gap of 100 bp
* * 22071218 221595: contig of 793 bp in length
* * 22151219 222395: gap of 100 bp
* * 22231220 223195: contig of 794 bp in length
* * 22311221 223995: gap of 100 bp
* * 22391222 224795: contig of 795 bp in length
* * 22471223 225595: gap of 100 bp
* * 22551224 226395: contig of 796 bp in length
* * 22631225 227195: gap of 100 bp
* * 22711226 227995: contig of 797 bp in length
* * 22791227 228795: gap of 100 bp
* * 22871228 229595: contig of 798 bp in length
* * 22951229 230395: gap of 100 bp
* * 23031230 231195: contig of 799 bp in length
* * 23111231 231995: gap of 100 bp
* * 23191232 232795: contig of 800 bp in length
* * 23271233 233595: gap of 100 bp
* * 23351234 234395: contig of 801 bp in length
* * 23431235 235195: gap of 100 bp
* * 23511236 235995: contig of 802 bp in length
* * 23591237 236795: gap of 100 bp
* * 23671238 237595: contig of 803 bp in length
* * 23751239 238395: gap of 100 bp
* * 23831240 239195: contig of 804 bp in length
* * 23911241 239995: gap of 100 bp
* * 23991242 240795: contig of 805 bp in length
* * 24071243 241595: gap of 100 bp
* * 24151244 242395: contig of 806 bp in length
* * 24231245 243195: gap of 100 bp
* * 24311246 243995: contig of 807 bp in length
* * 24391247 244795: gap of 100 bp
* * 24471248 245595: contig of 808 bp in length
* * 24551249 246395: gap of 100 bp
* * 24631250 247195: contig of 809 bp in length
* * 24711251 247995: gap of 100 bp
* * 24791252 248795: contig of 810 bp in length
* * 24871253 249595: gap of 100 bp
* * 24951254 250395: contig of 811 bp in length
* * 25031255 251195: gap of 100 bp
* * 25111256 251995: contig of 812 bp in length
* * 25191257 252795: gap of 100 bp
* * 25271258 253595: contig of 813 bp in length
* * 25351259 254395: gap of 100 bp
* * 25431260 255195: contig of 814 bp in length
* * 25511261 255995: gap of 100 bp
* * 25591262 256795: contig of 815 bp in length
* * 25671263 257595: gap of 100 bp
* * 25751264 258395: contig of 816 bp in length
* * 25831265 259195: gap of 100 bp
* * 25911266 259995: contig of 817 bp in length
* * 25991267 260795: gap of 100 bp
* * 26071268 261595: contig of 818 bp in length
* * 26151269 262395: gap of 100 bp
* * 26231270 263195: contig of 819 bp in length
* * 26311271 263995: gap of 100 bp
* * 26391272 264795: contig of 820 bp in length
* * 26471273 265595: gap of 100 bp
* * 26551274 266395: contig of 821 bp in length
* * 26631275 267195: gap of 100 bp
* * 26711276 267995: contig of 822 bp in length
* * 26791277 268795: gap of 100 bp
* * 26871278 269595: contig of 823 bp in length
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* * 27031280 271195: contig of 824 bp in length
* * 27111281 271995: gap of 100 bp
* * 27191282 272795: contig of 825 bp in length
* * 27271283 273595: gap of 100 bp
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* * 27431285 275195: gap of 100 bp
* * 27511286 275995: contig of 827 bp in length
* * 27591287 276795: gap of 100 bp
* * 27671288 277595: contig of 828 bp in length
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* * 27831290 279195: contig of 829 bp in length
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* * 28471298 285595: contig of 833 bp in length
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* * 28631300 287195: contig of 834 bp in length
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* * 28791302 288795: contig of 835 bp in length
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* * 29271308 293595: contig of 838 bp in length
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* * 29431310 295195: contig of 839 bp in length
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* * 29591312 296795: contig of 840 bp in length
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* * 29751314 298395: contig of 841 bp in length
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* * 30231320 303195: contig of 844 bp in length
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* * 31031330 311195: contig of 849 bp in length
* * 31111331 311995: gap of 100 bp
* * 31191332 312795: contig of 850 bp in length
* * 31271333 313595: gap of 100 bp
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* * 31511336 315995: contig of 852 bp in length
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* * 32151344 322395: contig of 856 bp in length
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* * 32551349 326395: gap of 100 bp
* * 32631350 327195: contig of 859 bp in length
* * 32711351 327995: gap of 100 bp
* * 32791352 328795: contig of 860 bp in length
* * 32871353 329595: gap of 100 bp
* * 32951354 330395: contig of 861 bp in length
* * 33031355 331195: gap of 100 bp
* * 33111356 331995: contig of 862 bp in length
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Search completed: October 21, 2001, 18:18:05
Job time: 26587 sec

